

In the Specification:

Please amend the specification without prejudice, as set forth below.

Please delete the title of the invention at line 4 on page 1 of the specification, and insert the following title in place thereof:

-- NOVEL FIBROBLAST GROWTH FACTOR (FGF23) AND
~~METHODS FOR USE NUCLEIC ACIDS~~ --

Please delete the paragraph beginning at line 11 of page 10 and ending at line 12 of page 10 and insert the following paragraph in place thereof:

-- Figure 9 is the amino acid sequence of human FGF23 (SEQ ID NO:2) where the predicted signal peptide and RXXR/S (SEQ ID NO:35) protease cleavage sites are indicated. --

Please delete the paragraph beginning at line 29 of page 44 and ending at line 12 of page 45 and insert the following paragraph in place thereof:

-- The determination of percent identity between two nucleotide or amino acid sequences can be accomplished using a mathematical algorithm. For example, a mathematical algorithm useful for comparing two sequences is the algorithm of Karlin and Altschul (1990, Proc. Natl. Acad. Sci. USA 87:2264-2268), modified as in Karlin and Altschul (1993, Proc. Natl. Acad. Sci. USA 90:5873-5877). This algorithm is incorporated into the NBLAST and XBLAST programs of Altschul, et al. (1990, J. Mol. Biol. 215:403-410), and can be accessed, for example, at the National Center for Biotechnology Information (NCBI) world wide web site having the universal resource locator "<http://www.ncbi.nlm.nih.gov/BLAST/>" <<www.ncbi.nlm.nih.gov/BLAST/>>. BLAST nucleotide searches can be performed with the NBLAST program (designated "blastn" at the NCBI web site), using the following parameters: gap penalty = 5; gap extension penalty = 2; mismatch penalty = 3; match reward = 1; expectation value 10.0;

and word size = 11 to obtain nucleotide sequences homologous to a nucleic acid described herein. BLAST protein searches can be performed with the XBLAST program (designated "blastn" at the NCBI web site) or the NCBI "blastp" program, using the following parameters: expectation value 10.0, BLOSUM62 scoring matrix to obtain amino acid sequences homologous to a protein molecule described herein. --

Please delete the paragraph beginning at line 13 of page 45 and ending at line 19 of page 45 and insert the following paragraph in place thereof:

-- To obtain gapped alignments for comparison purposes, Gapped BLAST can be utilized as described in Altschul et al. (1997, Nucleic Acids Res. 25:3389-3402). Alternatively, PSI-Blast or PHI-Blast can be used to perform an iterated search which detects distant relationships between molecules (Id.) and relationships between molecules which share a common pattern. When utilizing BLAST, Gapped BLAST, PSI-Blast, and PHI-Blast programs, the default parameters of the respective programs (e.g., XBLAST and NBLAST) can be used. See <http://www.ncbi.nlm.nih.gov>
<<www.ncbi.nlm.nih.gov>>. --